# FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCC**ATG**CACAAGGCGGGGCTGCTAGGCCTC

TGTGCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT

CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC

GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG

GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA

GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC

TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG

TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC

AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC

CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC

CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACTGCCTAGCACCTGGACTTATCAA

GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC

TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT

GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT

C**TGA**GGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCCTGC

ATTCACCCACTGGCCTTTCCCACCTCTGCTCACCTTACTGTTCACCTCATCAAATCAGTTCT

GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCCTGCT

GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT

GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCCTGGGCCACTGGTGAATCTGAGGGGTGA

TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG

TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAAA

# FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

# FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTCGAGGACCAGGCGGCG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCGAGACTTTCTGGCTGCGCTGGAGGACGCC**ATG**GAGCAGTACAAACTGC
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
CCAGGCTGGGGGGGCCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCCTTTGTGCCTCGACCTCATAC
AGCCCCCCTGGGGGGTGCCCACGCCCATGTGCTGGGCATGGTGCCGCCTGCCTGCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCCAG
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTCAGGCCCGCCAGGTCCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCGCTG
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCG
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
GAGATCGCGGCCTTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGGTGCTTCGGGCCTCAGCCTCGTTGCTGTCCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGTT
ACATGTGGATAAACCAGGAACTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTTCTCTGGCTGTCCCCCCTCACTGAGGGGGCCCCCCGCACCCGGGAGGAGACGCGGGACT
TGGTCCACGCTCCGTTACCCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC
GAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG
CCTGCCCTGGAACTTTGGGCCTTTGTCCAAGCCCCGGCGGGAACTGCGACGAGCCAGCCCGGGGATGA
TTGATGTCCGGAAAAACCCCCTG**TAA**GCCCTCGGGGCAGACCCTGCCTTGGAGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCAAAAGAACTGGACCCTCATTT
AACAAAATAATATGCAAATTCCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTCAGGGGTTTG
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAAATCTTTGAAGGGAC

# FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRLREETEQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSLLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSRGGEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

**Important features:**

**Leucine zipper pattern.**

amino acids 557-579, 794-815

**N-glycosylation sites.**

amino acids 133-136, 383-386

**Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

# FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGC**ATG**AGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT

GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA

CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG

CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT

TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG

AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGGAGCTGTAC

CAGGAACAGGAGGCACGTCCTGTACCCA**TAA**AAACCCCAGGCTCCACTGGCAGACGGCAGAC

AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA

ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC

CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG

AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

# FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS

LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP

**Important features:**

**Signal sequence**

amino acids 1-21

**N-myristoylation sites.**

amino acids 33-39, 70-76

# FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT

TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG

AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG

GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT

GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG

GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG

TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCGCGCCCGCCGCTGCTACCCCTG

CGCCCGCTGCGAGCCCGGCGTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG

GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCTCGGCCGCGCTCCCCGCCCGCCC

GCCCGCCGGGACGTGGTAGGGG**ATG**CCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA

GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG

AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG

CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT

GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC

TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC

CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCGGAACTCGCGCCCA

CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG

AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCTCGGCCTGCCCGTGCCT

GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA

TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC

CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG

TGAAGCCAACGGTGAGGTGCTATGCACAGTGTCAGCGTGTCCCCAGACGGAGTGTGTGGACC

CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA

ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC

TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC

AAATG**TAG**ACGCTTCCCAGAACACAAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA

CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA

TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTC

AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG

TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG

CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAAA

AAAAAAAAAAAAAAAAAAAA

# FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKSKSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAIGEKFAPGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

# FIGURE 9

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC

TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC

GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA

CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG

AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC

TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT

TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG

AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT

GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC

CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA

ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC

TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT

GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG

GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGG

GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG

CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTC

CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCCGAATGACCTGCCCCAGG

GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT

GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG

GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT

GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG

GTGGGGAGTGGTTTGCCCTTCCTGC**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA

CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC

CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA

ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG

GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

# FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174, 198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352, 360-365, 361-366, 388-393, 408-413, 419-424

# FIGURE 11

CGACG**ATG**CTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCTATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCTTCCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC
TTGCCGCCGCCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTGATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAAATGCTACAGCTCTTT
ATCACGTGGAAGCCTTCAAAACTGGACCAGAAATGCAGAACATTTTAAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
GCGTACAATTACAAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAAACTGTTTCA
TTTTATGAAGATCTGAAGAACCACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTA**TGA**GTAACTGAAGAACATTTTT
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTCATAATAACACTTGAAAAGTGCT
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACTTTAC
AGATTGTTCTGCAGTTCTCTCTTCTTTTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
TGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTTACTTCTAGGAAGTCTCAAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTCATTCTGT
CACTTGGCTTCGATTTTTATATTTTCCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATTCTTGTGACTTTAAAAAAAAA

# FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:**

**Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

# FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCTCAGCAACCCTCGAC**ATG**GCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGCATCATTACGGATTCGC
AGACAAGTGACCCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCCACGGATT
CCAGAGCCAATCCCAGATTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCACTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATC**TGA**GACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCCTGCTTGTCCAACAGGGTGTCAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCTTTTCT
CACACAAGTTTTAGCCTTTTTCACAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTAAAAGAAAATGGAT
CCCACTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTCACGCTCCAGCCTCCT
TCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAC
CTCATTTATAAAAGCTTCAAAAAAACCCA

# FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

# FIGURE 15

CAGGACCAGGTCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACC**ATG**CACATCCTCGTGGTCCATGCCATGGTG
ATCCTGCTGACGCTGGGCCCGCCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
GAGAAGCCACTGCCCACCGCCTTCCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTG
CGCATGATCCGTTCTGAGGTGCTCCGCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACTCCTCCAGTTCCTGGACCAGGCAGTGGCCCAC
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCACCTGGTGGAGGTCCAGCATGAGCGC
GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCCGCCGAGACAGCACAGAGGCA
CCCAAACCAAAGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTCGGGTGGGGACCCAGCTCCGGGTGCTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCCTCCAGATTTTCCCGCTCAGCCCGGACCCTCGGTGGCAGAGCTCC
AGTCCCCGCCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCGTCGTCCAGGGCAGCCCC
GAGGTGCCGGGCATCACGGTGCGTGTCCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG
CCACAGGACACCGGCTTCTCCTCGCTCTTCCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
GTGGAGGGCGGGCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGCGCAGGCTCAGTGAT
GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTCAGGACCTGGAGGTGGTCAGCTCCACCGTC
CGTGCCGTCATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCCTCCAG
GGGCTGATCGAGGTGAGGTCCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCTGGCTGGG
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCTCCTAGTGGACTGG
CTGGAAATGCTGGACCCCGAGGTGGTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGGAGGAAG
GGCAAAGGTCAGGCCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCTCTTCACGCATCAGTCCAGCTGGCCC
ACACTGCACCAGTGCATCCGAGTCCTGCTGGGCAAGAGCCGGGAACAGAGGTTCGACCCCTCTGCCTCTCTGGAC
TTCCTCTGGGCCTGCATCCATGTTCCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG
GAGCTGGTGCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
AGCCAGGACGGGGACACAGCCGCCTGCAGCCTCATCCAGGCCCGGCTGCCCCTGCTGCTCAGCTGCTGCTGTGGG
GACGATGAGAGTGTCAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGGAGACAGCGTGCTGGGA
AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCCGGAGCTGCGGGTGCCCGTGCCTGAGGTCCTA
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
GCGGACACCAGCGACTCCCGGGCGTTGGAGAACCGAGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC
CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCCTGCACGTGCTGGGCCTGCTGGAGCTGCTGCAGCCGCAC
GTGTTCCGCAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCCTTCATCCGCCTGCTGCTGAATTACAGG
AAGTCCTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGCAGTTCATCCATAAGTACATTACCTACAATGCC
CCAGCAGCCATCTCCTTCCTGCAGAAGCACGCCGACCCGCTCCACGACCTGTCCTTCGACAACAGTGACCTGGTG
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCTGGTCAGCGTCTCCCTGTTCACCCCTCTGACCGCGGCCGAG
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
GAGTGTTGCCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC
CTGCCCACGTTCATGTACTGCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCCTGGTGGGCATGTACGGCCAGATG
GACCCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATG**TGA**GCCTGTGGCAGCCGA
CCCCCCTCCAAGCCCCGGCCCGTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCCAGGAAGCGTGGGCGTTGCTGG
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCCAGGAGCAATACTCCGAGCCCTGGGGTGG
CTCCGGGCCGGCCGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG
AGCGGCGGATCCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

# FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRQLCQYQRCVPQDTGFSSLFLKVLLQMLQWLDSPG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPQKR
REELVLRVQGPELISLVELILAEAETRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE
HLSGCIQQWGDSVLGRRCRDLLLQLYLQRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMIAALLHGRTHLNFQEFRQQNHL
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNYRKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL
MSSAEECCRNLAFSLALRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

**Important features:**

**Signal peptide:**

amino acids 1-16

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

**N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449, 665-671, 698-704

**Amidation sites.**

amino acids 329-333, 634-638

# FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAG**ATG**AGGCTCCGC
AATGGCACCTTCCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCCTCTCGCTGTCCTGGTA
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCCTGGCGC
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGGCCGCCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTCGGTGGTGATGGGCATCCC
GAGCGTGCGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTCATCTCACCCTCCCCCCACTTCTACCCTGACTTCTCCCGCCTCCGAGAGTCCT
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA
TCCTGGAGTTCTCCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGCAGTGGGAACATCGAGCACCC
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCCTGAAAAAGGCCGAC**TAA**GCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA
GCCCACATTTCTGGGGGTGTCGTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAA
AGGGTTCTGCCTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCGGAGGCCCTA
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCC
TGAGGCCCGGAACCGTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAGAGCTTTTAC
TTGGGCGCCCGCCGTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT
TTTTATTCTTGGATACATTTGATTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

# FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVRWRTKQNLD
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

**Important features:**

**Signal sequence**

amino acids 1-23

**N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

**N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515